

EXHIBIT B



Databases Tools

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ClustalW2 Results

Results of search	
Number of sequences	4
Alignment score	9231
Sequence format	Pearson
Sequence type	aa
JalView	Start Jalview
Output file	clustalw2-20100803-1709277804.output
Alignment file	clustalw2-20100803-1709277804.aln
Guide tree file	clustalw2-20100803-1709277804.dnd
Your input file	clustalw2-20100803-1709277804.input
SUBMIT ANOTHER JOB	

To save a result file right-click the file link in the above table and choose "Save Target As".
If you cannot see the Jalview button, reload the page and check your browser settings to enable Java Applets.

Scores Table

Sort by		Sequence Number		View Output File	
SeqA Name	Len(aa)	SeqB Name	Len(aa)	Score	
1 Fischer_Phlp4>	10	2 SEQ#2>	500	30	
1 Fischer_Phlp4>	10	3 SEQ#4>	500	30	
1 Fischer_Phlp4>	10	4 SEQ#6>	500	30	
2 SEQ#2>	500	3 SEQ#4>	500	99	
2 SEQ#2>	500	4 SEQ#6>	500	92	
3 SEQ#4>	500	4 SEQ#6>	500	92	

PLEASE NOTE: Some scores may be missing from the above table if the alignment was done using multiple CPU mode. Please check the output.

Sort by		Sequence Number		View Output File	
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Alignment

Show Colors		View Alignment File	
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CLUSTAL 2.0.12 multiple sequence alignment

```
SEQ#2> YFPPPAKEDFLGCLVKEIPRLLYAKSSPAYPSVLGQTIIRNSRWSSPDNVKPIYIVTPT 60
SEQ#4> YFPPPAKEDFLGCLVKEIPRLLYAKSSPAYPSVLGQTIIRNSRWSSPDNVKPIYIVTPT 60
SEQ#6> YFPPPAKEDFLGCLVKEIPRLLYAKSSPAYPSVLGQTIIRNSRWSSPDNVKPIYIVTPT 60
Fischer_Phlp4> -----

SEQ#2> NASHIQSAVVCGRRHGVRIRVRSGGHDYEGLSYRSLQPEEFAVVDLSKMRVAVVDGKART 120
SEQ#4> NASHIQSAVVCGRRHGVRIRVRSGGHDYEGLSYRSLQPEEFAVVDLSKMRVAVVDGKART 120
SEQ#6> NVSHIQSAVVCGRRHGVRIRVRSGGHDYEGLSYRSLQPETFAVVDLNMRAVAVVDGKART 120
Fischer_Phlp4> -----

SEQ#2> AWVDSGAQLGELYAIHKASTVLAFPAVCPTIGVGGNFAGGGFGMLLRKYGIAAENVID 180
SEQ#4> AWVDSGAQLGELYAIHKASTVLAFPAVCPTIGVGGNFAGGGFGMLLRKYGIAAENVID 180
SEQ#6> AWVDSGAQLGELYAIKASPTLAFPAVCPTIGVGGNFAGGGFGMLLRKYGIAAENVID 180
Fischer_Phlp4> -----IVALPX-----G-----MLK----- 10
                          **: * *:

SEQ#2> VKLVDANGTLHDKKSMGDDHFWAVRGGGSGFGIVVAVKVRLLPVPTVTVFKIPKASE 240
SEQ#4> VKLVDANGTLHDKKSMGDDHFWAVRGGGSGFGIVVAVKVRLLPVPTVTVFKIPKASE 240
SEQ#6> VKLVDANGTLHDKKSMGDDHFWAVRGGGSGFGIVVAVKVRLLPVPTVTVFKISKVSE 240
Fischer_Phlp4> -----

SEQ#2> GAVDIINRWQVAPQLPDDLIRVIAQGPATFEAMYLGTCTLTPLMSSKFPELGMNAS 300
SEQ#4> GAVDIINRWQVAPQLPDDLIRVIAQGPATFEAMYLGTCTLTPLMSSKFPELGMNAS 300
SEQ#6> GAVDIINRWQVAPQLPADLMIRIIAQGPKATFEAMYLGTCTLTPLMSSKFPELGMNAS 300
Fischer_Phlp4> -----

SEQ#2> HCNEMSWIQSIPFVHLGHRDNIEDDLLNRNNTFKPFAEYKSDYVYEPFPPKRVWEQIFSTW 360
SEQ#4> HCNEMSWIQSIPFVHLGHRDNIEDDLLNRNNTFKPFAEYKSDYVYEPFPPKRVWEQIFSTW 360
SEQ#6> HCNEMSWIQSIPFVHLGHRDALEDLLNRNNSFKPFAEYKSDYVYQPPPKTVWEQILNTW 360
Fischer_Phlp4> -----

SEQ#2> LLKPGAGIMIFDPYGATISATPEWATFFPHRKGVLFIQVNVWFAPGAGAAPLSWSKEI 420
```

```
SEQ#2>          YNYMEPYVSKNPRQAYANYRDIDLGRNEVVNDVSTFSSGLVWGQKYFKGNFQRLAITKGK 480
SEQ#4>          YNYMEPYVSKNPRQAYANYRDIDLGRNEVVNDVSTFSSGLVWGQKYFKGNFQRLAITKGK 480
SEQ#6>          YNYMEPYVSKNPRQAYANYRDIDLGRNEVVNDVSTYASGKVWGQKYFKGNFERLAITKGK 480
Fischer_Phlp4>  -----
```

```
SEQ#2>          VDPTDYFRNEQSIPPLIKKY 500
SEQ#4>          VDPTDYFRNEQSIPPLIKKY 500
SEQ#6>          VDPTDYFRNEQSIPPLIKKY 500
Fischer_Phlp4>  -----
```

PLEASE NOTE: Showing colors on large alignments is slow.

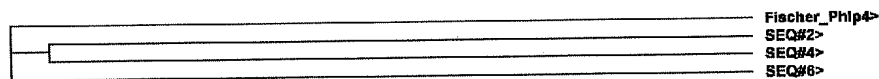
[Show Colors](#)[View Alignment File](#)

Guide Tree

[Show as Phylogram Tree](#)[Show Distances](#)[View DND File](#)

```
(
  Fischer_Phlp4>:0.66250,
  (
    SEQ#2>:0.00250,
    SEQ#4>:0.00150)
  :0.03550,
  SEQ#6>:0.03750);
```

Cladogram

[Show as Phylogram Tree](#)[Show Distances](#)[View DND File](#)

Right-click on the above tree to see display options.

Problems printing? Read [how to print a Phylogram or Cladogram](#).